Amendments to the Specification:

Please amend the specification by inserting the below paragraph before the first paragraph of the specification:

-- This application is a continuation of, and claims priority under 35 USC §120 to, US Application 09/944,396, abandoned, and is a continuation of, and claims priority under 35 USC § 120 to, US Application 09/866028 filed 5/25/2001, which is a continuation of, and claims priority under 35 USC §120 to, PCT Application PCT/US99/28301 filed 12/1/1999, which claims priority under 35 USC §119 to US Provisional Application 60/113296 filed 12/22/1998, where PCT/US99/28301 is a continuation-in-part of, and claims priority under 35 USC §120 to, US Application 09/254311 filed 3/3/1999, now abandoned, which is the National Stage filed under 35 USC §371 of PCT Application PCT/US98/25108 filed 12/1/1998, which claims priority under 35 USC §119 to US Provisional Application 60/069873 filed 12/17/1997.--

Please replace the paragraph beginning at page 25, line 8, with the following rewritten paragraph:

--Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). ~~The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov.~~ NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

Please replace the paragraph beginning on page 27, line 29, with the following paragraph:

--Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). ~~The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov.~~ NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.--

Please replace the paragraph beginning on page 94, line 16, with the following paragraph:

--EXAMPLE 4: Isolation of cDNA Clones Encoding Human PRO243 by Genomic Walking

Introduction: Human thrombopoietin (THPO) is a glocosylated hormone of 352 amino acids consisting of two domains. The N-terminal domain, sharing 50% similarity to erythropoietin, is responsible for the biological activity. The C-terminal region is required for secretion. The gene for thrombopoietin (THPO) maps to human chromosome 3q27-q28 where the six exons of this gene span 7 kilobase pairs of genomic DNA (Gurney *et al.*, *Blood* 85: 981-988 (1995). In order to determine whether there were any genes encoding THPO homologues located in close proximity to THPO, genomic DNA fragments from this region were identified and sequenced. Three P1 clones and one PAC clones (Genome Systems Inc., St. Louis, MO; cat. Nos. P1-2535 and PAC-6539) encompassing the THPO locus were isolated and a 140 kb region was sequenced using the ordered shotgun strategy (Chen *et al.*, *Genomics* U17:651-656 (1993)), coupled with a PCR-based gap filling approach. Analysis reveals that the region is gene0rich with four additional genes located very close to THPO: tumor necrosis factor-receptor type 1 associated protein 2 (TRAP2) and elongation initiation factor gamma (eIF4g), chloride channel 2 (CLCN2) and RNA polymerase II subunit hRPB17. While no THPO homolog was found in the region, four novel genes have been predicted by computer-assisted gene detection (GRAIL)(Xu *et al., Gen. Engin.*

16:241-253 (1994), the presence of CpG islands (Cross, S. and Bird, A., *Curr. Opin. Genet. & Devel.* 5: 109-314 (1995), and homology to known genes (as detected by WU-BLAST2.0)(Altschul and Gish, *Methods Enzymol.* 266:460-480 (1996) ~~(http://blast.wustl.edu/blast/README.html)~~.--

Please replace the paragraph beginning on page 95, line 11, with the following paragraph:

-- In order to define better the THPO locus and to search for other genes related to the hematopoietin family, four genomic clones were isolated from this region by PCR screening of human P1 and PAC libraries (Genome System, Inc., Cat. Nos.: P1-2535 and PAC-6539). The sizes of the genomic fragments are as follows: P1.t is 40 kb; P1.g is 70 kb; P1.u is 70 kb; and PAC.z is 200 kb. Approximately 80% of the 200 kb genomic DNA region was sequenced by the Ordered Shotgun Strategy (OSS) (Chen et al., Genomics 17: 651-56(1993), and assembled into contigs using ~~AutoAssembler~~ AUTOASSEMBLER™ (Applied Biosystems, Perkin Elmer, Foster City, Calif., cat. no. 903227). The preliminary order of these contigs was determined by manual analysis. There were 46 contigs and filling in the gaps was employed. Table 7 summarized the number and sizes of the gaps.--

Please replace the paragraph beginning on page 95, line 30, with the following paragraph:

-- *DNA sequencing:* ABI DYE-~~primer~~PRIMER™ chemistry (PE Applied Biosystems, Foster City, Calif.; Cat. No.: 402112) was used to end-sequence the lambda and plasmid subclones. ABI DYE-~~terminater~~TERMINATER™ chemistry (PE Applied Biosystems, Foster City, Calif., Cat. No: 403044) was used to sequence the PCR products with their respective PCR primers. The sequences were collected with an ABI377 instrument. For PCR products larger than 1 kb, walking primers were used. The sequences of contigs generated by the OSS strategy in ~~AutoAssembler~~ AUTOASSEMBLER™ a (PE Applied Biosystems, Foster City, Calif.; Cat. No: 903227)

and the gap-filling sequencing trace files were imported into ~~Sequencher~~ SEQUENCHER™ (Gene Codes Corp., Ann Arbor, Mich.) for overlapping and editing.--

Please replace the paragraph beginning on page 96, line 11, with the following paragraph:

--Analysis: The identification and characterization of coding regions was carried out as follows: First, repetitive sequences were masked using RepeatMasker (A. F. A. Smit & P. Green, unpublished results ~~http://ftp.genome.washington.edu/RM/RM_details.html~~) which screens DNA sequences in FastA format against a library of repetitive elements and returns a masked query sequence. Repeats not masked were identified by comparing the sequence to the GenBank database using WUBLAST (Altschul, S & Gish, W., Methods Enzymol. 266: 460-480 (1996) and were masked manually. –

Please replace the paragraph beginning on page 116, line 5, with the following paragraph:

-- Recombinant baculovirus is generated by co-transfecting the above plasmid and ~~BaculoGold~~BACULOGOLD™ virus DNA (Pharmingen) into Spodoptera frugiperda ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28ºC., the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual. Oxford: Oxford University Press (1994). --

Please replace the paragraph beginning on page 119, line 4 and continuing onto page 120 through line 6, with the following paragraph:

-- The starting material for the screen was genomic DNA isolated from a variety cancers. The DNA is quantitated precisely, e.g., fluorometrically. As a negative control, DNA was isolated from the cells of ten normal healthy individuals which was pooled and

used as assay controls for the gene copy in healthy individuals (not shown). The 5' nuclease assay (for example, ~~TaqMan~~TAQMAN™) and real-time quantitative PCR (for example, ABI Prizm 7700 ~~Sequence Detection System~~SEQUENCE DETECTION SYSTEM™ (Perkin Elmer, Applied Biosystems Division, Foster City, Calif.)), were used to find genes potentially amplified in certain cancers. The results were used to determine whether the DNA encoding PRO327, PRO344, PRO347, PRO357 or PRO715 is over-represented in any of the primary lung or colon cancers or cancer cell lines or breast cancer cell lines that were screened. The primary lung cancers were obtained from individuals with tumors of the type and stage as indicated in Table 9. An explanation of the abbreviations used for the designation of the primary tumors listed in Table 9 and the primary tumors and cell lines referred to throughout this example are given below.--

Please replace the paragraph beginning on page 120, line 7, with the following paragraph:

-- The results of the ~~TaqMan~~TAQMAN™ are reported in delta (Δ) Ct units. One unit corresponds to 1 PCR cycle or approximately a 2-fold amplification relative to normal, two units corresponds to 4-fold, 3 units to 8-fold amplification and so on. Quantitation was obtained using primers and a ~~TaqMan~~TAQMAN™ fluorescent probe derived from the PRO327-, PRO344-, PRO347-, PRO357- or PRO715-encoding gene. Regions of PRO327, PRO344, PRO347, PRO357 or PRO715 which are most likely to contain unique nucleic acid sequences and which are least likely to have spliced out introns are preferred for the primer and probe derivation, e.g., 3'-untranslated regions. The sequences for the primers and probes (forward, reverse and probe) used for the PRO327, PRO344, PRO347, PRO357 or PRO715 gene amplification analysis were as follows:--